

I. AMENDMENT

To the specification:

Please replace the paragraph on page 44, lines 14-20, with the following rewritten paragraph:

FIG. 1 presents nucleotide sequence (SEQ ID NO:9) and deduced amino acid sequence (SEQ ID NO:10) of *hpa* cDNA ~~with regard to SEQ ID NO: 11~~. A single nucleotide difference at position 799 (A to T) between the EST (Expressed Sequence Tag) and the PCR amplified cDNA (reverse transcribed RNA) and the resulting amino acid substitution (Tyr to Phe) are indicated above and below the substituted unit, respectively. Cysteine residues and the poly adenylation consensus sequence are underlined. The asterisk denotes the stop codon TGA.

Please replace the paragraph on page 51, lines 1-5, with the following rewritten paragraph:

FIG. 16 presents the nucleotide sequence of the genomic region of the *hpa* gene with regard to SEQ ID NO: 42. Exon sequences appear in upper case and intron sequences in lower case. The deduced amino acid sequence of the twelve exons is printed below the nucleotide sequence. These twelve deduced amino acids sequences are: positions 1 to 76 of SEQ ID NO:10 (exon 1); positions 77 to 124 of SEQ ID NO:10 (exon 2); positions 125 to 166 of SEQ ID NO:10 (exon 3); positions 167 to 224 of SEQ ID NO:10 (exon 4); positions 225 to 281 of SEQ ID NO:10 (exon 5); positions 282 to 297 of SEQ ID NO:10 (exon 6); positions 298 to 328 of SEQ ID NO:10 (exon 7); positions 329 to 364 of SEQ ID NO:10 (exon 8); positions 365 to 402 of SEQ ID NO:10 (exon 9); positions 403 to 442 of SEQ ID NO:10 (exon 10); positions 443 to 491 of SEQ ID NO:10 (exon 11); and positions 492 to 543 of SEQ ID NO:10 (exon 12). Two predicted transcription start sites are shown in bold.